0/07

#2



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RAW SEQUENCE LISTING

DATE: 01/30/2002

PATENT APPLICATION:

US/09/991,681

TIME: 17:26:06

Input Set : N:\Crf3\RULE60\09991681.txt
Output Set: N:\CRF3\01302002\1991681.raw

SEQUENCE LISTING

(1) GENERAL INFORMATION:

```
(i) APPLICANT: BILLING-MEDEL, PATRICIA
      7
                             COHEN, MAURICE
      8
                             COLPITTS, TRACEY L.
                                                                  ENTERED
      9
                             FRIEDMAN, PAULA N.
     10
                             GORDON, JULIAN
                             GRANADOS, EDWARD N.
     11
                             HODGES, STEVEN C.
     12
     13
                             KLASS, MICHAEL R.
     14
                             KRATOCHVIL, JON D.
     15
                             ROBERTS-RAPP, LISA
                             RUSSELL, JOHN C.
W--> 16
W--> 17
                             STROUPE, STEPHEN D.
            (ii) TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
C--> 19
     20
                                      FOR DETECTING DISEASES OF THE PROSTATE
     22
           (iii) NUMBER OF SEQUENCES: 33
     24
            (iv) CORRESPONDENCE ADDRESS:
                   (A) ADDRESSEE: Abbott Laboratories
     25
     26
                   (B) STREET: 100 Abbott Park Road
     27
                   (C) CITY: Abbott Park
     28
                   (D) STATE: IL
     29
                   (E) COUNTRY: USA
                   (F) ZIP: 60064-3500
     30
             (V) COMPUTER READABLE FORM:
     32
     33
                   (A) MEDIUM TYPE: Diskette
                   (B) COMPUTER: IBM Compatible
     34
                   (C) OPERATING SYSTEM: DOS
     35
                   (D) SOFTWARE: FastSEQ for Windows Version 2.0
     36
     38
            (vi) CURRENT APPLICATION DATA:
C--> 39
                   (A) APPLICATION NUMBER: US/09/991,681
C--> 40
                   (B) FILING DATE: 26-Nov-2001
     41
                   (C) CLASSIFICATION:
     43
           (vii) PRIOR APPLICATION DATA:
                   (A) APPLICATION NUMBER: 09/065,383
     44
     45
                   (B) FILING DATE:
          (viii) ATTORNEY/AGENT INFORMATION:
     49
     50
                   (A) NAME: Becker, Cheryl L.
                   (B) REGISTRATION NUMBER: 35,441
     51
     52
                   (C) REFERENCE/DOCKET NUMBER: 6084.US.P1
     54
            (ix) TELECOMMUNICATION INFORMATION:
     55
                  (A) TELEPHONE: 847/935-1729
     56
                  (B) TELEFAX: 847/938-2623
```

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PATENT APPLICATION: US/09/991,681

57		(C) TELEX:						
62	(2)	INFORMATION FOR SEQ ID NO: 1:						
64		(i) SEQUENCE CHARACTERISTICS:						
65		(A) LENGTH: 232 base pairs						
66		(B) TYPE: nucleic acid						
67		(C) STRANDEDNESS: single						
68		(D) TOPOLOGY: linear						
		· · ·						
71		(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:	60					
73		GGCGCATCCG AGCCATGGCC CAGCAGGTGT TTATGCTGGA CACCCAGTGC TCACCAAAGA						
74		CACCAAACAA CTTTGACCAC GCTCAGTCCT GCCAGCTCAT TATTGAGCTG CCTCCTGATG	120					
75		AAAAACCAAA TGGACACACC AAGAAAAGCG TGTCTTTCAG GGAAATTGTG GTGAGCCTGC	180					
76		TGTCTCATCA GGTGTTACTC CAGAACTTAT ATGACATCTT GTTAGAAGAG TT	232					
· 78	(2)	INFORMATION FOR SEQ ID NO: 2:						
80		(i) SEQUENCE CHARACTERISTICS:						
81		(A) LENGTH: 289 base pairs						
82		(B) TYPE: nucleic acid						
. 83		(C) STRANDEDNESS: single						
84		(D) TOPOLOGY: linear						
87		(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:						
89		CTTTCAGGGA AATTGTGGTG AGCCTGCTGT CTCATCAGGT GTTACTCCAG AACTTATATG	60					
90		ACATCTTGTT AGAAGAGTTT GTCAAAGGCC CCTCTCCTGG AGAGGAAAAG ACGATACAAG	120					
91		TGCCAGAAGC CAAGCTGGCT GGCTTCCTCA GATACATCTC TATGCAGAAC TTGGCAGTCA	180					
		TATTCGACCT GCTGCTGGAC TCTTATAGGA CTGCCAGGGA GTTTGACACC AGCCCCGGGC	240					
.92		TGAAGTGCCT GCTGAAGAAA GTGTCTGGCA TCGGGGGCGC CGCCAACCT	289					
93			209					
95		INFORMATION FOR SEQ ID NO: 3:						
97	• •	(i) SEQUENCE CHARACTERISTICS:						
98		(A) LENGTH: 264 base pairs						
99		(B) TYPE: nucleic acid						
100		(C) STRANDEDNESS: single						
. 101	Ĺ	(D) TOPOLOGY: linear						
104	Į.	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:						
106	5 .	GGCAGTCATA TTCGACCTGC TGCTGGACTC TTATAGGACT GCCAGGGAGT TTGACACCAG	, 6 0					
107	7	CCCCGGCTG AAGTGCCTGC TGAAGAAAGT GTCTGGCATC GGGGGCGCCG CCAACCTCTA	120					
108	3	CCGCCAGTCT GCGATGAGTT TAACATTTAT TTCCACGCCC TGGTGTGTGC TGTTCTCACC	180					
109		AATCAAGAAA ACATCACGGC CGAGCAAGTG AAGAAGGTCC TTTTTGAGGA CGACGAGAGA	240					
110		AGCACGGATT CTTCCCAGCA GTGT	264					
112	2. (2) INFORMATION FOR SEQ ID NO: 4:						
114	•	(i) SEQUENCE CHARACTERISTICS:						
115		(A) LENGTH: 260 base pairs						
116		(B) TYPE: nucleic acid						
117		(C) STRANDEDNESS: single						
118		(D) TOPOLOGY: linear						
121		(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:	60					
123		CATATTCGAC CTGCTGCTGG ACTCTTATAG GACTGCCAGG GAGTTTGACA CCAGCCCCGG	60					
124		GCTGAAGTGC CTGCTGAAGA AAGTGTCTGG CATCGGGGGC GCCGCCAACC TCTACCGCCA	120					
125		GTCTGCGATG AGCTTTAACA TTTATTTCCA CGCCCTGGTG TGTGCTGTTC TCACCAATCA	180					
126		AGAAACCATC ACGGCCGAGC AAGTGAAGAA GGTCCTTTTT GAGGACGACG AGAGAAGCAC	240					
127		GGATTCTTCC CAGCAGTGTT	260					
129	(2)	INFORMATION FOR SEQ ID NO: 5:						

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131		(i) SEQUENCE CHARACTERISTICS:						
132		(A) LENGTH: 199 base pairs						
133		(B) TYPE: nucleic acid						
134		(C) STRANDEDNESS: single						
135		(D) TOPOLOGY: linear						
138		(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:	60					
140		CCACTGGGTC CCAGGGGCCA GGACTCCCCG CIGCITCAGC GIGCOCHOON GILLONG	.20					
141		CAAGGGCAAA TGCGGCATTC CITCAGCGCA GGCCCCGAGC TGCTGCGAGC	.80					
142		CCCCGCTCAG GCTCCACCGG GAGCTCCCTC AGTGTCTCGG TGAGAAAAA						
143		ATCAGGCATG GACCAACAT 199						
145	(2)	INFORMATION FOR SEQ ID NO: 6:						
147		(i) SEQUENCE CHARACTERISTICS:						
148		(A) LENGTH: 470 base pairs						
149		(B) TYPE: nucleic acid						
150		(C) STRANDEDNESS: single						
151		(D) TOPOLOGY: linear						
154		(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6: CATTCCTTCA GEGCAGGCCC CGAGCTGCTG CGACAGGACA AGAGGCCCCG CTCAGGCTCC	60					
156		CAPTCCTTCA GEGEAGGEE CGAGCIGCIG CGACAGACA MONOGOGGG GIGING	L20					
157		ACCIGINATION COUNTRICATION CHOICE COUNTRICATION CONTRICTOR COUNTRICTOR COUNTRI	L80					
158		AACATGGTGC TAACAGTTCT CAATCAGATT CAGATTCTCC CAGTGGTGTG	240					
159		CPCCAGCCCG CAGTGTTCCC GIGCATCAGT CAGCTGACCT GIGHTGTGTG	300					
160		TAGCCGACTC CTGTTCTACT CTCCCACCAA ATAACAGTAG TGAGGGTTAG AGTCCTGCCA	360					
161		TAGINGALIN, CIGITETACI CICCOCCOM MILMONOTIO ISSUED	120					
162		GAACAGTGTT TCCTAATGTA AAAAGCCTTT CCAACCACTG ATCAGCATTA	170					
163	(2)	INFORMATION FOR SEQ ID NO: 7:						
167	(2)	(i) SEQUENCE CHARACTERISTICS:						
168		(A) LENGTH: 232 base pairs						
169		(B) TYPE: nucleic acid						
170		(C) STRANDEDNESS: single						
171		(D) TOPOLOGY: linear						
174		(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:						
176		CACGGCCCTC CAGCCCGCAG TGTTCCCGTG CATCAGTCAG CTGACCTGTC ACGTGACCGA	60					
177		CATCAGAGTT CGCCAGGCIG IGAGGGAGIG GCIGGGCAGG GIGGGGGG	120					
178		CATTGTGTAG CCGACICCIG IICIACICIC COMOGNATIO	180					
179		CCTGCCAATA CAGCTGTTGC ATTITCCCCA CCACTAGGGG CHCTTMMIGT III	232					
181	(2)	INFORMATION FOR SEQ ID NO: 8:						
183	•	(i) SEQUENCE CHARACTERISTICS:						
184		(A) LENGTH: 244 base pairs						
185		(B) TYPE: nucleic acid						
186		(C) STRANDEDNESS: single						
187		(D) TOPOLOGY: linear						
190		(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:	60					
192		TAAGGTTTGT ATCTAGATGA CACAAACGAT ATTCTGATTT TGCACATTAT TATAGAAGAA	120					
193		TCTATAATCC TTGATATGII ICIAACICII GAAGIAIAII 1000A01001	180					
194		GTGTTGTCCC CAAATGGGTC ATTITCAAGG ATTITCTCATT	240					
195		ATTTGATCCA TCATTTAAAA AATAAATACA ATTGGTAAGG	244					
196		AGCT	•					
198	(2)	INFORMATION FOR SEQ ID NO: 9:						

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DATE: 01/30/2002 TIME: 17:26:06

	(i) SEQUENCE CHARACTERISTICS:						
200	(1) SEQUENCE CHARACTERISTICS.						
201	(A) LENGTH: 1771 base pairs						
202	(B) TYPE: nucleic acid						
203	(C) STRANDEDNESS: single						
204	(D) TOPOLOGY: linear						
207	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:						
209	GGCAGTCATA TTCGACCTGC TGCTGGACTC TTATAGGACT GCCAGGGAGT TTGACACCAG	120					
210	CCCCGGGCTG AAGTGCCTGC TGAAGAAAGT GTCTGGCATC GGGGGCGCCG CCAACCTCTA						
211	CCGCCAGTCT GCGATGAGCT TTAACATTTA TTTCCACGCC CTGGTGTGTG CTGTTCTCAC	180					
212	CAATCAAGAA ACCATCACGG CCGAGCAAGT GAAGAAGGTC CTTTTTGAGG ACGACGAGAG	240					
213	AAGCACGGAT TCTTCCCAGC AGTGTTCATC TGAGGATGAA GACATCTTTG AGGAAACCGC	300					
214	CCAGGTCAGC CCCCCGAGAG GCAAGGAGAA GAGACAGTGG CGGGCACGGA TGCCCTTGCT	360					
215	CAGCGTCCAG CCTGTCAGCA ACGCAGATTG GGTGTGGCTG GTCAAGAGGC TGCACAAGCT	420					
216	GTGCATGGAA CTGTGCAACA ACTACATCCA GATGCACTTG GACCTGGAGA ACTGTATGGA	480					
217	GGAGCCTCCC ATCTTCAAGG GCGACCCGTT CTTCATCCTG CCCTCCTTCC AGTCCGAGTC	540					
218	ATCCACCCA TCCACCGGGG GCTTCTCTGG GAAAGAAACC CCTTCCGAGG ATGACAGAAG	600					
219	CCAGTCCCGG GAGCACATGG GCGAGTCCCT GAGCCTGAAG GCCGGTGGTG GGGACCTGCT	660					
220	GCTGCCCCC AGCCCCAAAG TGGAGAAGAA GGATCCCAGC CGGAAGAAGG AGTGGTGGGA	720					
221	GAATGCGGGG AACAAAATCT ACACCATGGC AGCCGACAAG ACCATTTCAA AGTTGATGAC	780					
221	CGAATACAAA AAGAGGAAAC AGCAGCACAA CCTGTCCGCG TTCCCCAAAG AGGTCAAAGT	840					
	GGAGAAGAAA GGAGAGCCAC TGGGTCCCAG GGGCCAGGAC TCCCCGCTGC TTCAGCGTCC	900					
223 224	CCAGCACTTG ATGGACCAAG GGCAAATGCG GCATTCCTTC AGCGCAGGCC CCGAGCTGCT	960					
	GCGACAGGAC AAGAGGCCCC GCTCAGGCTC CACCGGGAGC TCCCTCAGTG TCTCGGTGAG	1020					
225	AGACGCAGAA GCACAGATCC AGGCATGGAC CAACATGGTG CTAACAGTTC TCAATCAGAT	1080					
226	TCAGATTCTC CCAGACCAGA CCTTCACGGC CCTCCAGCCC GCAGTGTTCC CGTGCATCAG	1140					
227	TCAGCTGACC TGTCACGTGA CCGACATCAG AGTTCGCCAG GCTGTGAGGG AGTGGCTGGG	1200					
228	CAGGGTGGC CGTGTCTATG ACATCATTGT GTAGCCGACT CCTGTTCTAC TCTCCCACCA	1260					
229	AATAACAGTA GTGAGGGTTA GAGTCCTGCC AATACAGCTG TTGCATTTTC CCCACCACTA	1320					
230	GCCCCACTTA AACTACTACT ACTGTCTCAG AGAACAGTGT TTCCTAATGT AAAAAGCCTT	1380					
231	TCCAACCACT GATCAGCATT GGGGCCATAC TAAGGTTTGT ATCTAGATGA CACAAACGAT	1440					
232	ATTCTGATTT TGCACATTAT TATAGAAGAA TCTATAATCC TTGATATGTT TCTAACTCTT	1500					
233	GAAGTATAT TCCCAGTGCT TTTGCTTACA GTGTTGTCCC CAAATGGGTC ATTTTCAAGG	1560					
234	ATTACTCATT TGAAAACACT ATATTGATCC ATTTGATCCA TCATTTAAAA AATAAATACA	1620					
235	ATTACTCATT TGAAAACACT ATATTGATCC ATTTGATCCA TCATTTAAAA AATAAATACA	1680					
236	ATTCCTAAGG CAATATCTGC TGGTAAGTCA AGCTGATAAA CACTCAGACA TCTAGTACCA	1740					
237	GGGATTATTA ATTGGAGGAA GATTTATGGT TATGGGTCTG GCTGGGAAGA AGACAACTAT	1771					
238	AAATACATAT TCTTGGGTGT CATAATCAAG A	1//1					
240	(2) INFORMATION FOR SEQ ID NO: 10:						
242	(i) SEQUENCE CHARACTERISTICS:						
243	(A) LENGTH: 2096 base pairs						
244	(B) TYPE: nucleic acid	•					
245	(C) STRANDEDNESS: single						
246	(D) TOPOLOGY: linear						
249	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:						
251	GGCGCATCCG AGCCATGGCC CAGCAGGTGT TTATGCTGGA CACCCAGTGC TCACCAAAGA	60					
252	CACCAAACAA CTTTGACCAC GCTCAGTCCT GCCAGCTCAT TATTGAGCTG CCTCCTGATG	120					
253	AAAAACCAAA TGGACACCC AAGAAAAGCG TGTCTTTCAG GGAAATTGTG GTGAGCCTGC	180					
254	TGTCTCATCA GGTGTTACTC CAGAACTTAT ATGACATCTT GTTAGAAGAG TTTGTCAAAG	240					
255	GCCCCTCTCC TGGAGAGGAA AAGACGATAC AAGTGCCAGA AGCCAAGCTG GCTGGCTTCC	300					
256	TCAGATACAT CTCTATGCAG AACTTGGCAG TCATATTCGA CCTGCTGCTG GACTCTTATA	360					

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					aamaamaa		420
257	GGACTGCCAG GGA						420
258	GCATCGGGGG CGC						480
259	ACGCCCTGGT GTG						540
260	AGGTCCTTTT TGA						600
261	ATGAAGACAT CTT					•	660
262	AGTGGCGGGC ACG						720
263	GGCTGGTCAA GAG						780
264	ACTTGGACCT GGA						840
265	TCCTGCCCTC CTT				•	·	900
266	AAACCCCTTC CGA						960
267	TGAAGGCCGG TGG						1020
268	CCAGCCGGAA GAA						1080
269	ACAAGACCAT TTC	CAAAGTTG	ATGACCGAAT	ACAAAAAGAG	GAAACAGCAG	CACAACCTGT	1140
270	CCGCGTTCCC CAA	AAGAGGTC	AAAGTGGAGA	AGAAAGGAGA	GCCACTGGGT	CCCAGGGGCC	1200
271	AGGACTCCCC GCT	rgcttcag	CGTCCCCAGC	ACTTGATGGA	CCAAGGGCAA	ATGCGGCATT	1260
272	CCTTCAGCGC AGG	GCCCCGAG	CTGCTGCGAC	AGGACAAGAG	GCCCCGCTCA	GGCTCCACCG	1320
273	GGAGCTCCCT CAG	STGTCTCG	GTGAGAGACG	CAGAAGCACA	GATCCAGGCA	TGGACCAACA	1380
274	TGGTGCTAAC AGT	TTCTCAAT	CAGATTCAGA	TTCTCCCAGA	CCAGACCTTC	ACGGCCCTCC	1440
275	AGCCCGCAGT GTT	TCCCGTGC	ATCAGTCAGC	TGACCTGTCA	CGTGACCGAC	ATCAGAGTTC	1500
276	GCCAGGCTGT GAG	GGAGTGG	CTGGGCAGGG	TGGGCCGTGT	CTATGACATC	ATTGTGTAGC	1560
277	CGACTCCTGT TCT	PACTCTCC	CACCAAATAA	CAGTAGTGAG	GGTTAGAGTC	CTGCCAATAC	1620
278	AGCTGTTGCA TTT	TTCCCCAC	CACTAGCCCC	ACTTAAACTA	CTACTACTGT	CTCAGAGAAC	1680
279	AGTGTTTCCT AAT	IGTAAAAA	GCCTTTCCAA	CCACTGATCA	GCATTRGGGC	CATACTAAGG	1740
280	TTTGTATCTA GAT	rgacacaa	ACGATATTCT	GATTTTGCAC	ATTATTATAG	AAGAATCTAT	1800
281	AATCCTTGAT ATG	GTTTCTAA	CTCTTGAAGT	ATATTTCCCA	GTGCTTTTGC	TTACAGTGTT	1860
282	GTCCCCAAAT GGG	STCATTTT	CAAGGATTAC	TCATTTGAAA	ACACTATATT	GATCCATTTG	1920
283	ATCCATCATT TAA	AAAAATAA	ATACAATTCC	TAAGGCAATA	TCTGCTGGTA	AGTCAAGCTG	1980
284	ATAAACACTC AGA	ACATCTAG	TACCAGGGAT	TATTAATTGG	AGGAAGATTT	ATGGTTATGG	2040
285	GTCTGGCTGG GAA	GAAGACA	ACTATAAATA	CATATTCTTG	GGTGTCATAA	TCAAGA	2096
	INFORMATION FO						
289	(i) SEQUENCE						
290	• •		ase pairs				
291	• •	E: nuclei	_				
292			: single				
293		DLOGY: li					
296	(xi) SEQUENCE). NO: 11:			
298	AGCTCGGAAT TCC				GACTAGTGAG	CTCGTCGACC	60
299	CGGGAATT		0001010		0010100	02002001100	68
		OR SEO ID	NO 12				•
301 (2)	INFORMATION FOR SEQ ID NO: 12: (i) SEQUENCE CHARACTERISTICS:						
304	* *		ase pairs				
305		E: nuclei					
306	• •			•			
307	(C) STRANDEDNESS: single						
307	(D) TOPOLOGY: linear						
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12: AATTAATTCC CGGGTCGACG AGCTCACTAG TCGGCGGCCG CTCTAGAGGA TCCAAGCTCG 6						
312							
313							
	2) INFORMATION FOR SEQ ID NO: 13: (i) SEQUENCE CHARACTERISTICS:						
317	(1) SEQUENCE	CHARACTE	KISTICS:				=

VERIFICATION SUMMARY DATE: 01/30/2002
PATENT APPLICATION: US/09/991,681 TIME: 17:26:07

Input Set : N:\Crf3\RULE60\09991681.txt
Output Set: N:\CRF3\01302002\1991681.raw

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L:19 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:39 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:40 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:16 M:259 W: Allowed number of lines exceeded, (i) APPLICANT:
L:17 M:259 W: Allowed number of lines exceeded, (i) APPLICANT:
L:505 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27
L:584 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=28
L:603 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=29
L:622 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=30
L:641 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=31